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| | L30 | L29 | 9 | | | |
| | DB=PGPB, USPT; PLUR=YES; OP=OR | | | | | |
| | L29 | briand-jacques.in. | 9 | | | |
| | L28 | L11 and L27 | 0 | | | |
| | L27 | (enzyme and product) with NMR | 118 | | | |
| | L26 | 5804390.pn. or 5698401.pn. | 2 | | | |
| | L25 | 5804390.pn | . 0 | | | |
| | L24 | isotop\$ and 119 | 1 | | | |
| | L23 | (1H or 3H or 11B or 13C or 15N or 19F or 29S or 31P) and L22 | 0 | | | |
| | L22 | L21 | 1 | | | |
| | L21 | chemical adj shift and L19 | 1 | | | |
| | L20 | chemical ajd shift and L19 | 898333 | | | |
| | L19 | 20030143757.pn. | 1 | | | |
| | DB=PGPB, USPT, USOC, EPAB, JPAB, DWPI, TDBD; PLUR=YES; OP=OR | | | | | |
| | L18 | 6150179.pn. | 2 | | | |
| | DB=USPT; PLUR=YES; OP=OR | | | | | |
| | L17 | 6150179.pn. | 1 | | | |
| | DB=EPAB; $PLUR=YES$; $OP=OR$ | | | | | |
| | L16 | WO-9857155-A1.did. | 1 | | | |
| | L15 | WO-9857155-A1.did. | 1 | | | |
| | DB = PGPB, USPT, USOC, EPAB, JPAB, DWPI, TDBD; PLUR = YES; OP = OR | | | | | |
| | L14 | L13 not 110 | 1 | | | |
| | L13 | L11 and L12 | 5 | | | |
| | L12 | (substrate or ligand) with NMR | 1730 | | | |
| | L11 | NMR with (one adj dimension\$ adj spectr\$ or two adj dimension\$ adj spectr\$ or three adj dimension\$ adj spectr\$) | 35 | | | |
| | DB=PGPB, $USPT$; $PLUR=YES$; $OP=OR$ | | | | | |
| | L10 | L7 and L9 | 4 | | | |
| | L9 | NMR with (one adj dimension\$ adj spectr\$ or two adj dimension\$ adj spectr\$ or three adj dimension\$ adj spectr\$) | 29 | | | |
| | L8 | L5 and L7 | 238 | | | |

| Search I | Page 2 of 2 | | |
|----------|-------------|--|-------|
| | | | |
| | L7 | (substrate or ligand) with NMR | 1579 |
| | L6 | 12 and L5 | 355 |
| | L5 | NMR with (one adj dimension\$ or two adj dimension\$ or three adj dimension\$) | 2019 |
| | L4 | NMR same (one adj dimension\$ or two adj dimension\$ or three adj dimension\$) | 3112 |
| | L3 | 11 AND L2 | 1303 |
| | L2 | (substrate or ligand) same NMR | 4300 |
| | L1 | NMR and (one adj dimension\$ or two adj dimension\$ or three adj dimension\$) | 12089 |

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L1
=> s nmr and (substrate or ligand or enzyme)
         64621 NMR AND (SUBSTRATE OR LIGAND OR ENZYME)
=> s 11 and 12
         49788 L1 AND L2
L3
=> e briand jacques/in
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'IN' IS NOT A VALID EXPAND FIELD CODE FOR FILE 'EMBASE'
                  BRIAND J M/IN
            1
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            20
                   BRIAND J P/IN
E2
E3
            4 --> BRIAND JACQUES/IN
E4
            1
                   BRIAND JEAN/IN
E5
            1
                   BRIAND JEAN J/IN
                   BRIAND JEAN PAUL/IN
Е6
            19
                   BRIAND JEAN PIERRE/IN
E7
            3
E8
            8
                 BRIAND L/IN
E9
            3
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=> e briand jacques/au
           579
                   BRIAND J P/AU
E1
                   BRIAND J Y/AU
E2
            1
            24 --> BRIAND JACQUES/AU
E3
                   BRIAND JEAN/AU
E4
            1
                   BRIAND JEAN CLAUDE/AU
E5
             1
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E6
            11
                   BRIAND JEAN J/AU
E7
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                   BRIAND JEAN P/AU
E8
            11
                   BRIAND JEAN PAUL/AU
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                   BRIAND JEAN PIERRE/AU
E10
            27
E11
            12
                   BRIAND JOEL/AU
E12
            18
                   BRIAND K/AU
=> s e3
L4
            24 "BRIAND JACQUES"/AU
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2 DUP REM L5 (1 DUPLICATE REMOVED)

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L6 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN

Mechanism of Inhibition of Cathepsin K by Potent, Selective TI 1,5-Diacylcarbohydrazides: A New Class of Mechanism-Based Inhibitors of Thiol Proteases

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Design of potent and selective human cathepsin K inhibitors that span the TΤ active site.

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ANSWER 1 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER:

1999:709526 CAPLUS

DOCUMENT NUMBER:

132:44920

TITLE: -

Mechanism of Inhibition of Cathepsin K by Potent, Selective 1,5-Diacylcarbohydrazides: A New Class of

Mechanism-Based Inhibitors of Thiol Proteases

AUTHOR(S):

Bossard, Mary J.; Tomaszek, Thaddeus A.; Levy, Mark

A.; Ijames, Carl F.; Huddleston, Michael J.; Briand, Jacques; Thompson, Scott; Halpert, Stacie; Veber, Daniel F.; Carr, Steven A.; Meek,

Thomas D.; Tew, David G.

CORPORATE SOURCE:

Departments of Molecular Recognition Physical and Structural Chemistry and Medicinal Chemistry,

SmithKline Beecham Pharmaceuticals, King of Prussia,

PA, 19406, USA

SOURCE:

Biochemistry (1999), 38(48), 15893-15902

CODEN: BICHAW; ISSN: 0006-2960

PUBLISHER:

American Chemical Society

DOCUMENT TYPE:

Journal

English LANGUAGE:

The nature of the inhibition of thiol proteases by a new class of AΒ mechanism-based inhibitors, 1,5-diacylcarbohydrazides, is described. These potent, time-dependent, active-site spanning inhibitors include compds. that are selective for cathepsin K, a cysteine protease unique to osteoclasts. The 1,5-diacylcarbohydrazides are slow substrates for members of the papain superfamily with inhibition resulting from slow enzyme decarbamylation. Enzyme-catalyzed hydrolysis of 2,2'-N,N'-bis(benzyloxycarbonyl)-L-leucinylcarbohydrazide is accompanied by formation of a hydrazide-containing product and a carbamyl-enzyme intermediate that is sufficiently stable to be observed by mass spectrometry and NMR. Stopped-flow studies yield a saturation limited value of 43

s-1 for the rate of cathepsin K acylation by 2,2'-N,N'bis(benzyloxycarbonyl)-L-leucinylcarbohydrazide. Inhibition potency varies among proteases tested as reflected by 2-3 orders of magnitude differences in Ki and kobs/I, but all eventually form the same stable covalent intermediate. Reactivation rates are equivalent for all enzymes tested (1 + 10-4 s-1), indicating hydrolysis of a common carbamyl-enzyme form. NMR spectroscopic studies with cathepsin K and 2,2'-N,N'-bis(benzyloxycarbonyl)-L-leucinylcarbohydrazide provide evidence of inhibitor cleavage to generate a covalent carbamyl-enzyme intermediate rather than a tetrahedral complex. The product Cbz-Leu-hydrazide does not appear enzyme-bound after cleavage in the NMR spectra, suggesting that the stable inhibited form of the enzyme is the thioester complex. 1,5-Diacylcarbohydrazides represent a new class of unreactive cysteine protease inhibitors that share a common mechanism of action across members of the papain superfamily. Both S and S' subsite interactions are exploited in achieving high selectivity and potency.

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DUPLICATE 1

1998:82491 BIOSIS ACCESSION NUMBER: PREV199800082491 DOCUMENT NUMBER:

Design of potent and selective human cathepsin K inhibitors TITLE:

that span the active site.

Thompson, Scott K.; Halbert, Stacie M.; Bossard, Mary J.; AUTHOR(S):

Tomaszek, Thaddeus A.; Levy, Mark A.; Zhao, Baoguang; Smith, Ward W.; Abdel-Meguid, Sherin S.; Janson, Cheryl A.; D'Alessio, Karla J.; McQueney, Michael S.; Amegadzie, Bernard Y.; Hanning, Charles R.; Desjarlais, Renee L.;

Briand, Jacques; Sarkar, Susanta K.; Huddleston,

Michael J.; Ijames, Carl F.; Carr, Steven A.; Garnes, Keith T.; Shu, Art; Heys, J. Richard; Bradbeer, Jeremy; Zembryki, Denise; Lee-Rykaczewski, Liz; James, Ian E.; Lark, Michael W.; Drake, Fred H.; Gowen, Maxine; Gleason, John G.; Veber,

Daniel F. [Reprint author]

Dep. Medicinal Chem., SmithKline Beecham Pharm., 709 CORPORATE SOURCE:

Swedeland Road, P.O. Box 1539, King Prussia, PA 19406, USA

Proceedings of the National Academy of Sciences of the SOURCE:

United States of America, (Dec. 23, 1997) Vol. 94, No. 26,

pp. 14249-14254. print.

CODEN: PNASA6. ISSN: 0027-8424.

DOCUMENT TYPE:

Article English

LANGUAGE: ENTRY DATE:

Entered STN: 24 Feb 1998

Last Updated on STN: 24 Feb 1998

Potent and selective active-site-spanning inhibitors have been designed AΒ for cathepsin K, a cysteine protease unique to osteoclasts. They act by mechanisms that involve tight binding intermediates, potentially on a hydrolytic pathway. X-ray crystallographic, MS, NMR spectroscopic, and kinetic studies of the mechanisms of inhibition indicate that different intermediates or transition states are being represented that are dependent on the conditions of measurement and the specific groups flanking the carbonyl in the inhibitor. The species observed crystallographically are most consistent with tetrahedral intermediates that may be close approximations of those that occur during substrate hydrolysis. Initial kinetic studies suggest the possibility of irreversible and reversible active-site modification. Representative inhibitors have demonstrated antiresorptive activity both in vitro and in vivo and therefore are promising leads for therapeutic agents for the treatment of osteoporosis. Expansion of these inhibitor

concepts can be envisioned for the many other cysteine proteases implicated for therapeutic intervention.

=> d his

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3 S L4 AND L1 L_5

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